

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model  
Run on: February 16, 2005, 16:12:05 ; Search time 168.877 Seconds  
(without alignments)  
2810.909 Million cell updates/sec  
Title: US-10-003-356-8  
Perfect score: 4904  
Sequence: 1 MFERRKEQDEGPGIHFLAF.....TVSTVLDLDRVLIYMCPLKIQ 927

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues  
Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0  
Maximum DB seq length: 20000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt\_03:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3962	80.8	912	2	O70410
2	2980	60.8	755	2	Q8NGV9
3	2296.5	46.8	618	2	Q8C0V4
4	1749	35.7	365	2	Q8TDU1
5	1727	35.2	428	2	O70413
6	1695.5	34.6	1085	1	CASR_BOVIN
7	1693.5	34.5	476	2	Q8C0M6
8	1691.5	34.5	1079	2	Q8OZA8
9	1690.5	34.5	1079	1	CASR_RAT
10	1688.5	34.4	1027	2	Q8JI04
11	1687.5	34.4	1078	1	CASR_HUMAN
12	1685.5	34.4	1079	1	CASR_MOUSE
13	1630.5	33.2	940	2	Q90WL6
14	1630.5	33.2	941	2	Q6XAF1
15	1629.5	33.2	941	2	Q6XAF3
16	1614	32.9	940	2	O73635
17	1609.5	32.8	880	2	O73639
18	1594.5	32.5	850	2	Q6XAF2
19	1551.5	31.6	848	2	O93553
20	1529	31.2	856	2	O73638
21	1497	30.5	864	2	O73637
22	1437	29.3	868	2	O73636
23	1417.5	28.9	854	2	Q6UNX3
24	1390	28.3	844	2	O93552
25	1332.5	27.2	875	2	O73640
26	1108.5	22.6	783	2	Q8CDP3
27	1074	21.9	855	2	O70409
28	1071	21.8	928	2	Q8K4Z6
29	1066	21.7	928	2	Q70VB1
30	1063	21.7	926	2	Q8NHZ9
31	1062	21.7	855	2	Q6TAC4

32	1017	20.7	879	2	Q8NGU8	Q8ngu8 homo sapien
33	990	20.2	877	2	Q9PW88	Q9pw88 carassius a
34	974.5	19.9	855	2	Q6JK43	Q6jk43 homo sapien
35	964	19.7	865	2	Q80Z09	Q80z09 mus musculu
36	961	19.6	779	2	O35269	O35269 rattus norv
37	955	19.5	842	2	Q99PG5	Q99pg5 mus musculu
38	950	19.4	842	2	Q92515	Q92515 mus musculu
39	943	19.2	842	2	Q923J9	Q923j9 mus musculu
40	942	19.2	840	2	Q9Z0R8	Q9z0r8 rattus norv
41	940.5	19.2	888	2	Q767K3	Q767k3 xenopus lae
42	939	19.1	842	2	Q99PG6	Q99pg6 mus musculu
43	912	18.6	866	2	O35268	O35268 rattus norv
44	904.5	18.4	230	2	O70414	O70414 rattus norv
45	901.5	18.4	751	2	Q6JK44	Q6jk44 homo sapien

ALIGNMENTS

RESULT 1  
O70410  
ID O70410 PRELIMINARY; PRT; 912 AA.  
AC O70410;  
DT 01-AUG-1998 (TREMBlrel. 07, Created)  
DT 01-AUG-1998 (TREMBlrel. 07, Last sequence update)  
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)  
DE Putative pheromone receptor V2R2.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Vomeronasal neurons;  
RX MEDLINE=97436753; PubMed=9292726; DOI=10.1016/S0896-6273(00)80946-0;  
RA Ryba N.J., Tirindelli R.;  
RT "A new multigene family of putative pheromone receptors.";  
RL Neuron 19:371-379(1997).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Vomeronasal neurons;  
RA Ryba N.J.P., Tirindelli R.;  
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF053986; AAC08413.1; -.  
DR HSSP; P23385; IEWK.  
DR GO; GO:0016020; C:membrane; IEA.  
DR GO; GO:0008067; F:metabotropic glutamate, GABA-B-like recepto. . .; IEA.  
DR GO; GO:0004872; F:receptor activity; IEA.  
DR InterPro; IPR001828; ANF\_receptor.  
DR InterPro; IPR000068; Ca\_sens\_receptor.  
DR InterPro; IPR000337; GPCR\_Mgr.  
DR InterPro; IPR011500; NCD3G\_GPCR.  
DR Pfam; PF00003; 7tm\_3; 1.  
DR Pfam; PF01094; ANF\_receptor; 1.  
DR Pfam; PF07562; NCD3G; 1.  
DR PRINTS; PR00592; CASENSINGR.  
DR PRINTS; PR00248; GPCR\_MGR.  
DR PROSITE; PS50259; G\_PROTEIN\_RECEP\_F3\_4; 1.  
KW Receptor.  
SQ SEQUENCE 912 AA; 102348 MW; 2C54FAB6DFBFA48D CRC64;

Query Match. 80.8%; Score 3962; DB 2; Length 912;  
Best Local Similarity 82.6%; Pred. No. 2e-270;  
Matches 747; Conservative 62; Mismatches 87; Indels 8; Gaps 2;  
Qy 17 FLAFLWAEILGSEAKEEKEERTCLIGK-----CVDAENHSLVIGLFPIDSR TIPANES 71  
||| ||| ||| : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| : |||  
Db 12 FLAFLWAVLGA---QNKTEEVQCRMLMAKFNLSGYVDKKNHSLVIAGLFP IHSRIIPVDEA 68  
Qy 72 ILEPASAKCEGFNFQFRFMWKAMIHMKIKNKRKDILPNITLGYQIFDTCFTISKSV EAV 131  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| : |||  
Db 69 ILEPVSPMCCEGFNFRGFRWMKMTMIHTIKERKDKILPNHTLGVQIFDSCYTISKAMESS 128

QY	132	LVFLTGEBNRPNFRNSTGAFPA	GIVGAGGSFLSVPASRIILGLYYLPQVG	YTS	TCVILSD	191		
Db	129	LVFLTGQBEFKPNFRNSTGST	LAALVSGSGSSLSVAASRIILGLYYMPQVG	YTS	SSCILSD	188		
QY	192	KYQFPSYLRVIASDKIQSKAVVKRI	QHFGWVWGAI	AADDYGYKVKT	FKKMESANLC	251		
Db	189	KYQFPSYLRVLPSDNLQSEAI	VNLIKHFGWVWGAI	AADDYGYKVKT	FKKMESANLC	248		
QY	252	VAFSETIPKVSNEKMOKAVKAVKT	STAKVIVLYTSDIDL	SLFVLEMIHNT	TDR	311		
Db	249	VAFSETIPKVSNEKMOKAVKAVKT	STAKVIVLYTSDIDL	SLFVLEMIHNT	TDR	308		
QY	312	EAWITSALIAKPEYFPYFGGT	IGFATPRSVIPGLKEFLYDVHPNKP	NDVLT	IEFWQTAF	371		
Db	309	EAWITSALIAKPEYFPYFGGT	IGFATPRSVIPGLKEFLYDVHPNKP	NDVLT	IEFWQTAF	368		
QY	372	NCTWPNSSVPYNVDHRVNMTG	KEDRLYDMSDQLCTGEEKLED	KNTYLDTSQLRIT	KQCK	431		
Db	369	NCTWPNSSVPYNVDHRVNMTG	KEDRLYDMSDQLCTGEEKLED	KNTYLDTSQLRIT	KQCK	428		
QY	432	QAVYAI	AHGLDHL	SRCQEGQGP	FGSNQQCAYIPTDFWQ	LMYYMKEIKFKSHEDKWILD	491	
Db	429	QAVYAI	AHGLDHL	SRCQEGQGP	FGSNQQCAYIPTDFWQ	LMYYMKEIKFKSHEDKWILD	488	
QY	492	DNGDLKNGHYDVLNWHLD	DEGEISFVTVGRF	NFRSTNFELV	IPTNSTIFWNT	ESSRLPHS	551	
Db	489	DNGDLKNGHYDVLNWHLD	DEGEISFVTVGRF	NFRSTNFELV	IPTNSTIFWNT	ESSRRPDS	548	
QY	552	VCTDVCBPGTGRGVQREPI	CCFDSIPCADGHVSRKPGERECE	QCAGEDYWSNAQ	KSECVL	611		
Db	549	FCTQVCBPGTRKGI	RGQOPICCFDCIPCADGYVSEKSGQRECD	PCGEDDWSNAGK	SKCVP	608		
QY	612	KEVEYL	AYDEALGFTLVILSV	FGAFVVLAVTAVYV	IHRHTPLVNASDWQLG	FLIQVSLII	671	
Db	609	KLVEFL	AYGEALGFTLVILSIF	GALVVLAVTVVYV	IHRHTPLVKANDRELS	FLIQMSLVI	668	
QY	672	MLSSMLFIDKPHNWS	CMAGQVTLALGFS	LCLSCLLGKTSSLFLAYRISK	SKTOL	SMHP	731	
Db	669	TVLSSLLFIGKPCNWS	CMARQITLALGFC	LCLSSILGKTISLFFAYRISV	SKTOL	ISMHP	728	
QY	732	LYRKII	VLISVLA	EIGICTAYLILEPPMVYKNMESQNTKI	ILGCNEISIEFLYS	MEGIDA	791	
Db	729	IFRKLIVLVCVVG	IGVCAAYLVEPPRMFKNIEIQNVKII	PECNEGVSVEFLCSIF	GF	FDV	788	
QY	792	FLALLCFL	TTFVARQLPDNYVEG	CITFGMLVFFI	IWMSFVPVYLSTKGKFK	MAVEIFAI	851	
Db	789	LRALLCFL	TTFVARQLPDNYVEG	CITFGMLVFFI	IVMISFVPAYLSTKGKFK	MAVEIFAI	848	
QY	852	LASSHGL	LGCI	FAPKCLII	LLRPERNTSEIV	CGRVSTTDNCIQLTSAFVSSEL	NNTTVST	911
Db	849	LASSYGL	LGCLFL	PKCFIILLR	PKRNTDET	VGGRVPTVDRSIQLTSASVSSEL	NNTTVST	908
QY	912	VLDD	915					
Db	909	VLDE	912					

## RESULT 2

QBNGV9				
ID	QBNGV9	PRELIMINARY;	PRT;	755 AA.
AC	QBNGV9;			
DT	01-OCT-2002	(TREMBlrel. 22,	Created)	
DT	01-OCT-2002	(TREMBlrel. 22,	Last sequence update)	
DT	01-JUN-2003	(TREMBlrel. 24,	Last annotation update)	
DE	Seven transmembrane helix receptor.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Euthera; Primates; Catarhini; Homnidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Suwa M., Sato T., Okouchi I., Arita M., Futami K., Matsumoto S.,			
RA	Teutsumi S., Aburatani H., Asai K., Akiyama Y.;			

Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
 EMBL; AB065664; BAC05890.1; -.  
 GO: GO:0016021; C:integral to membrane; IEA.  
 GO: GO:0008067; F:metabotropic glutamate, GABA-B-like recepto. . .; IEA.  
 GO: GO:0004872; F:receptor activity; IEA.  
 InterPro; IPR001828; ANF receptor.  
 InterPro; IPR000337; GPCR\_Mgr.  
 Pfam; PF00003; 7tm\_3; 1.  
 Pfam; PF01094; ANF receptor; 1.  
 PRINTS; PR00248; GPCRMR.  
 PROSITE; PS02529; G\_PROTEIN\_RECEP\_F3\_4; 1.  
 Receptor; Transmembrane.  
 KW SEQUENCE 755 AA; 83791 MW; 04D56AD8917BDA1F CRC64;

Query Match 60.8%; Score 2980; DB 2; Length 755;  
 Best Local Similarity 66.1%; Pred.No. 2.7e-201;  
 Matches 621; Conservative 34; Mismatches 88; Indels 196; Gaps 13;

QY	1	MFERRKEQDEGPGIHEFLAFLWAELGSEAKKEEERTCRLLGKCVDAENHSLVIGGLFP	60
Dd	1	MFERRKEQDEGPGIHEFLAFLWAELGSEAKKEEERTCRLLGKCVDAENHSLVIGGLFP	60
QY	61	IDSRTIPANESILEPASAKCEGFNFRWMKAMIHMIKEINKRKDILPNITLGYQIFDT	120
Dd	61	IDSRTIPANESILEPASAKCEGFNFRWMKAMIHMIKEINKRKDILPNITLGYQIFDT	120
QY	121	CFTTISKSVAEAVLVLTGQEEENRPNFRNSTGAPGAGIVGAGGSFSLVPASRIILGLYYLPQV	180
Dd	121	CFTTISKSVAEAVLVLTGQEEENRPNFRNSTGAPGAGIVGAGGSFSLVPASRIILGLYYLPQV	180
QY	181	GYSTCVILSDKYQFPSYLRLVIASDKIQSKAVVKRIQHFGVWVGAIADDDYKGYGKVT	240
Dd	181	GYSTCVILSDKYQFPSYLRLVIASDKIQSKAVVKRIQHFGVWVGAIADDDYKGYGKVT	240
QY	241	FKEMESANLCVAFSETIPKVYSNEKMQKAVKAVKTSTAKVIVLTSIDLSLFVLEMIH	300
Dd	224	LSPRLCSGAILA-----	237
QY	301	HNITDRTWIATEAWITSALIAKPEYFPYFGGTIGFATPRSVIPGLKEFLYDVHPNKPND	360
Dd	238	GNL-----	240
QY	361	VLTIETWQTAFNCTWPNSSVPYNDHRVNMVTGKEDRLYDMSDQLC-TGEKLEDLKNTYL	419
Dd	241	CLPVE-----TG-----FCHVAQAQGLEFLASNYL	264
QY	420	DTSQLRTKQCKQAVYAIAGHLDHLSRCQEGQPGFGSNQQCAYITPFDWQL---MYMK	476
Dd	265	TASASQ-----SAGITGVSH-----CAWPSITELMIQFHIYFRM	299
QY	477	EIKFKSHEDKWVILDDNGDLKNGHYDVLNWHLDDGEISFV--TVGRFNFRSTNFEVIP	534
Dd	300	NCRVTTERSVMLEYSGEISAHCHCLLGSSNSPASAPLVAGTTGAHHAQLIFVFLVE	359
QY	535	TNSTIFWNTESSRLPHSV-----CTDVCP-PGTGRGFVQREPICCFDSIPCADGHVSRKP	588
Dd	360	TG---FHHVSQDGLDLSIFPIQCVLMCVLLGLGRGFVQREPICCFDSIPCADGHVSRKP	416
QY	589	GERECECGEDYWSNAQKSECVLKEVEYLAYDEALGFTLVILSVFGAFVVLAVTAVYVIH	648
Dd	417	GERECECGEDYWSNAQKSECVLKEVEYLAYDEALGFTLVILSVFGAFVVLAVTAVYVIH	476
QY	649	RHTPLVNASDWQLGFLIQVSLIIMLLSSMLFIDKPHNWSMAGQVTLALGFSCLCLLG	708
Dd	477	RHTPLVNASDWQLGFLIQVSLIIMLLSSMLFIDKPHNWSMAGQVTLALGFSCLCLLG	536
QY	709	KTSSLFLAYRISKSTQLTSMHPLYRKIIIVLSVLAIEIGICTAYLILEPPMVYKMMESQN	768
Dd	537	KTSSLFLAYRISKSTQLTSMHPLYRKIIIVLSVLAIEIGICTAYLILEPPMVYKMMESQN	596
QY	769	TKIILGCNEISIEFLYSMFGIDAFLLALLCFLTTFVARQLPDNYEKGKCTTFGMLVFFIIW	828
Dd	597	TKIILGCNEISIEFLYSMFGIDAFLLALLCFLTTFVARQLPDNYEKGKCTTFGMLVFFIIW	656





```
RESULT 4
Q8TDUI PRELIMINARY; PRT; 365 AA.
AC Q8TDUI1;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Putative G-protein coupled receptor.
GN Name=GPCR;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
SEQUENCE FROM N.A.
RA Takeda S., Kadowaki S., Haga T., Takaesu H., Mitaku S.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB083610; BAB89323.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0008067; F:metabotropic glutamate, GABA-B-like recepto. . .; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR000337; GPCR_Mgr.
DR Pfam; PF00003; 7tm_3; 1.
DR PRINTS; PR00248; GPCR_MGR.
DR PROSITE; PS50259; G_PROTEIN_RECEP_F3_4; 1.
KW Receptor.
SQ SEQUENCE 365 AA; 40920 MW; 9BFC4F8EFA873133 CRC64;
Query Match 35.7%; Score 1749; DB 2; Length 365;
Best Local Similarity 99.1%; Pred. No. 6.5e-115;
Matches 341; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 584 VSRKPGERECEQCQGEDYWSNAQSECVLKEVEYLAYDEALGFTLVILSVFGAFVVLAVTA 643
DB 22 VLRSIGERECEQCQGEDYWSNAQSECVLKEVEYLAYDEALGFTLVILSVFGAFVVLAVTA 81
QY 644 VYVHRHTPLVNASDWQLGFLIQVSLIIMLSSMLFIDKPHNWSMAGQVTLALGFSCL 703
DB 82 VYVHRHTPLVNASDWQLGFLIQVSLIIMLSSMLFIDKPHNWSMAGQVTLALGFSCL 141
QY 704 SCLLGTSSFLAYRISKSTQLTSMHPLYRKIIIVLSVLAIEIGICTAYLILEPPMVYKN 763
DB 142 SCLLGTSSFLAYRISKSTQLTSMHPLYRKIIIVLSVLAIEIGICTAYLILEPPMVYKN 201
QY 764 MESQNTKIILGCNEISIEFLYSMFGIDAFALLCFLTTFVARQLPDNYYEGKCITFGMLV 823
DB 202 MESQNTKIILGCNEISIEFLYSMFGIDAFALLCFLTTFVARQLPDNYYEGKCITFGMLV 261
QY 824 FFIWMSFVPVYLTGKFKMAVEIFAILASSHGLLGICIFAPKCLILLRPERNTSEIVC 883
DB 262 FFIWMSFVPVYLTGKFKMAVEIFAILASSHGLLGICIFAPKCLILLRPERNTSEIVC 321
QY 884 GRVSTTDNCIQLTSFVSSELNNTTVSVTLDDRVLIMCPLKLQ 927
DB 322 GRVSTTDNCIQLTSFVSSELNNTTVSVTLDDRVLIMCPLKLQ 365
```

```
RESULT 5
O70413 PRELIMINARY; PRT; 428 AA.
AC O70413;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Putative pheromone receptor V2R2 (Fragment).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OC NCBI_TaxID=10116;
RN [1]
SEQUENCE FROM N.A.
RP TISSUE=Vomerol nasal neurons;
RC MEDLINE=97436753; PubMed=9292726; DOI=10.1016/S0896-6273(00)80946-0;
RX
```

```
RA Ryba N.J., Tirindelli R.;
RT "A new multigene family of putative pheromone receptors.";
RL Neuron 19:371-379(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Vomerol nasal neurons;
RA Ryba N.J.P., Tirindelli R.;
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF053989; AAC08416.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0008067; F:metabotropic glutamate, GABA-B-like recepto. . .; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR000337; GPCR_Mgr.
DR InterPro; IPR011500; NCD3G_GPCR.
DR Pfam; PF00003; 7tm_3; 1.
DR Pfam; PF07562; NCD3G; 1.
DR PRINTS; PR00248; GPCR_MGR.
DR PROSITE; PS50259; G_PROTEIN_RECEP_F3_4; 1.
KW Receptor.
FT NON TER 1
SQ SEQUENCE 428 AA; 47708 MW; EFB69A78F750E202 CRC64;
Query Match 35.2%; Score 1727; DB 2; Length 428;
Best Local Similarity 76.4%; Pred. No. 2.9e-113;
Matches 327; Conservative 40; Mismatches 61; Indels 0; Gaps 0;
QY 488 VILDDNGDLKNGHYDVLNWLHDDGEISFVTVGRFNRSTNFELVPTNSTIFWNTSSR 547
DB 1 VVLDNGDLKFGHYDILNWLQDDSGEISFVTVGRFNFKTDFELIPTNSTIFWNTSSR 60
QY 548 LPHSVCTDVCPPGTGRGFVQREPICCFDSIPCADGHVSRKPGERECEQCQGEDYWSNAQS 607
DB 61 RPSDFCTQVCPPGTRKGIQGGPICCFDCIPCADGYVSENPQRECDPCGEDDWSNAKS 120
QY 608 ECVLKEVEYLAYDEALGFTLVILSVFGAFVVLAVTAVYVHRHTPLVNASDWQLGFLIQV 667
DB 121 KCVFKLVEFLAYEEALGFTLVILSIFGALVVLAVTVVYVYRHTPLVKANDRELSFLIQM 180
QY 668 SLIIMLSSMLFIDKPHNWSMAGQVTLALGFSCLLGTSSFLAYRISKSTQLT 727
DB 181 SLVITVLSMLFIGKSCNWTQMARQVTLALGFCLSLTLGKTISLFFAYRISKSTRLI 240
QY 728 SMHPLYRKIIIVLSVLAIEIGICTAYLILEPPMVYKNMESQNTKIILGCNEISIEFLYSMF 787
DB 241 SMSPIYRKLIIVLCVVGIEGCAAYLVLEPPRMFKNIEPNVKIIFECNEGSIIEFLCAIF 300
QY 788 GIDAFALLCFLTTFVARQLPDNYYEGKCITFGMLVFFIWMSPVYVLTGKFKMAVE 847
DB 301 GFDVFLALLCFLTTFVARQLPDNYYEGKCITFGMLVFFIWMSPVYVLTGKFKMAVE 360
QY 848 IFAILASSHGLLGICIFAPKCLILLRPERNTSEIVCGRVSTTDNCIQLTSFVSSELNNT 907
DB 361 IFAILASSYGLLGICIFLPKCFIILLRPRKNTDETGVGRVPTVDRSIQLTSASVSELNNT 420
QY 908 TVSTVLDD 915
DB 421 AVSTVLDE 428
```

```
RESULT 6
CASR_BOVIN STANDARD; PRT; 1085 AA.
ID CASR_BOVIN
AC P35384;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Extracellular calcium-sensing receptor precursor (CaSR) (Parathyroid
DE Cell calcium-sensing receptor).
GN Name=CaSR; Synonyms=GPRC2A, PCAR1;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
```

OX NCBI\_TaxID=9913;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Parathyroid;  
RX MEDLINE=94077182; PubMed=8255296; DOI=10.1038/366575a0;  
RA Brown E.M., Gamba G., Riccardi D., Lombardi M., Butters R., Kifor O.,  
RA Sun A., Hediger M.A., Lytton J., Hebert S.C.;  
RT "Cloning and characterization of an extracellular Ca(2+)-sensing  
RT receptor from bovine parathyroid.";  
RL Nature 366:575-580(1993).  
CC -!- FUNCTION: Senses changes in the extracellular concentration of  
CC calcium ions. The activity of this receptor is mediated by a G-  
CC protein that activates a phosphatidylinositol-calcium second  
CC messenger system.  
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
CC -!- SIMILARITY: Belongs to the G-protein coupled receptor 3 family.  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (See [http://www.isb-sib.ch/](http://www.isb-sib.ch/announce/)  
CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
DR EMBL; S67307; AAB29171.1; -.  
DR PIR; S40476; S40476.  
DR HSSP; P23385; LEWT.  
DR InterPro; IPR001828; ANF receptor.  
DR InterPro; IPR000068; Ca\_sens\_receptor.  
DR InterPro; IPR000337; GPCR\_Mgr.  
DR Pfam; PF00003; 7tm\_3; 1.  
DR Pfam; PF01094; ANF\_receptor; 1.  
DR PRINTS; PR00248; GPCR\_MGR.  
DR PROSITE; PS00979; G\_PROTEIN\_RECEP\_F3\_1; 1.  
DR PROSITE; PS00980; G\_PROTEIN\_RECEP\_F3\_2; 1.  
DR PROSITE; PS00981; G\_PROTEIN\_RECEP\_F3\_3; 1.  
DR PROSITE; PS02529; G\_PROTEIN\_RECEP\_F3\_4; 1.  
KW G-protein coupled receptor; Glycoprotein; Signal; Transmembrane.  
FT SIGNAL 1 19  
FT CHAIN 20 1085 Extracellular calcium-sensing receptor.  
FT DOMAIN 20 613 Extracellular (Potential).  
FT TRANSMEM 614 636 1 (Potential).  
FT DOMAIN 637 650 Cytoplasmic (Potential).  
FT TRANSMEM 651 671 2 (Potential).  
FT DOMAIN 672 682 Extracellular (Potential).  
FT TRANSMEM 683 701 3 (Potential).  
FT DOMAIN 702 725 Cytoplasmic (Potential).  
FT TRANSMEM 726 746 4 (Potential).  
FT DOMAIN 747 770 Extracellular (Potential).  
FT TRANSMEM 771 793 5 (Potential).  
FT DOMAIN 794 806 Cytoplasmic (Potential).  
FT TRANSMEM 807 829 6 (Potential).  
FT DOMAIN 830 837 Extracellular (Potential).  
FT TRANSMEM 838 863 7 (Potential).  
FT DOMAIN 864 1085 Cytoplasmic (Potential).  
FT CARBOHYD 91 91 N-linked (GlcNAc... ) (Potential).  
FT CARBOHYD 131 131 N-linked (GlcNAc... ) (Potential).  
FT CARBOHYD 262 262 N-linked (GlcNAc... ) (Potential).  
FT CARBOHYD 288 288 N-linked (GlcNAc... ) (Potential).  
FT CARBOHYD 401 401 N-linked (GlcNAc... ) (Potential).  
FT CARBOHYD 447 447 N-linked (GlcNAc... ) (Potential).  
FT CARBOHYD 469 469 N-linked (GlcNAc... ) (Potential).  
FT CARBOHYD 489 489 N-linked (GlcNAc... ) (Potential).  
FT CARBOHYD 542 542 N-linked (GlcNAc... ) (Potential).  
FT CARBOHYD 595 595 N-linked (GlcNAc... ) (Potential).  
SQ SEQUENCE 1085 AA; 121170 MW; 5D66D8C9CD13B47 CRC64;  
  
Query Match 34.6%; Score 1695.5; DB 1; Length 1085;  
Best Local Similarity 39.3%; Pred. No. 1.7e-110;  
Matches 350; Conservative 173; Mismatches 323; Indels 45; Gaps 15;  
  
QY 53 LVIGGLFPIDSRTPANESI-LEPASAKCEGFNFQFRFWKAMTHMIKEINKRKDILPNI 111

Db 33 IILGGLFPIHFGVAVKQDLKSRPESVEICIRYFRGRWLQAMIFAEEINSSPALLPNM 92  
QY 112 TLGYQIPDTCFTISKSVAVLFLTCQE--ENRPNERNSTGAFPA--GIVGAGGSFLSV 166  
Db 93 TLGYRIFDTCNTVSKALEATLSFAQNKIDSLNDEFNCSEHIPSTIAVVGATGSGIST 152  
QY 167 PASRILGLYYLPQVGTYTSTCVILSDKYQPPSYLRVIAADKIQSKAVVKRIQHFQWVWGA 226  
Db 153 AVANLLGLFYIPQVSYASSRLLSNKNQPKSFLRTIPNDEHQATAMADIIEYFRWNWGT 212  
QY 227 IAADDYGYKYGKTFKEKMSANLCVAFSETIPKYSNEQMOKAVKAVKTSTAKVIVLYT 286  
Db 213 IAADDYGRPGIEKFREEAEERDIDFSELISQYSDEEKIQQVVEIQNSTAKVIVVFS 272  
QY 287 SDIDLSLFVLEMIHNNITDRTIATEAWITSALIAKPEYFPYFGGTIGFATPRSVIPGLK 346  
Db 273 SGPDLPLIKBIVRNITGRWLASEAWASSSLIAMPEYFHVVGTTIGFGLKAGQIPGFR 332  
QY 347 BFLVDHPNKPNDVLTIEFWQAFNC-TWPNSSVPYVNDHRVNMVTGKBDRLYDMSDQ-- 403  
Db 333 EFLQVHPKSVHNGFAKEFWETFNCHLQEGAKPLPD--TFLRGHEEGGARLSNSPT 390  
QY 404 ---LCTGEEKLEDLKNTYLTSQLRITKQCKQAVYAIAGHLHLSRCQEGQGFSGNQ 459  
Db 391 AFRPLCTGEENISSVETPYMDYTHLRISYNYLAVYSIAHLQDIYTCIPGRGLF-TNGS 449  
QY 460 CAYPTDFWQLMYMKEIKFKSHEDKWVILDDNGDLKNGHYDVNLNWLHD-DEGEISFVT 518  
Db 450 CADIKKVEAWQVLKHLRHLNFTSNMGEQVTFDECGDLA-GNYSIINWHLSPEDGSI VFKE 508  
QY 519 VGRNFRSTNFELVPTNSTIFWNTESSRLPHSVCTDVCPPGTGRGFVQREPICCFDSIP 578  
Db 509 VGYNVYAKKGERLFINDEKILWSGFSREVPFNSCRDCLAGTRKGIIEGEPTCCFECVE 568  
QY 579 CADGHVSRKPGERECEQCAGEDYWSNAQSECVLKEVEYLAVDEALGFTLVLSVFGAFVV 638  
Db 569 CPDGEYSDETDASACDKCPDDFSNENHTSCIAKEIEFLSWTEPFGIALTLFAVLGIFLT 628  
QY 639 LAVTAVYVHRHTPLVNASDNLGFLIQVSLIIMLLSSMLFIDKPHNWSMAGQVTLALG 698  
Db 629 AFVLGVFIKFRNTPIVKATNRELSYLLLSLLCCFSSSLFFICEPDQDWTCLRQPAFGIS 688  
QY 699 FSLCLSLGKTSSLFLAYRISKSTQLTSMHPLYRK-----IIVLSVLAIEGICT 750  
Db 689 FVLCISILVKTNRVLLVF--EAKIP-TSFH--RKWGLNLQFLVFLCTFMQIVICA 741  
QY 751 AYLILEPPMVYKNMESQNTKIILGCNEISIEFLYSMFGIDAFALLCFLTTFVARQLPDN 810  
Db 742 IWLNTAPPSSYRNHEDEIIFITCHEGSLMALGLIGYTCLLAAICFFFAFKSRKLLEN 801  
QY 811 YVEGKCITFGMLVFFIWMSPVVPVYVLTSGKFKMAVEIFAILASSHGLLGCIFAPKCLII 870  
Db 802 FNEAKFITFSMLIFFIVWISFIPAYASTYGFVSAVEVIAILAAISFGLLACIFFENKVYII 861  
QY 871 LLRPERNTSEIVCGRVSTTDNCIQLTSAFV-----SSELNNTTVST 911  
Db 862 LFKPSRNTIEEV--RCSTAHAHAFKVAARATLRRSNVSRQSRSSSLGGSTGST 910  
  
RESULT 7  
Q8COM6 PRELIMINARY; PRT; 476 AA.  
ID Q8COM6;  
AC Q8COM6;  
DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Mus musculus adult male testis cDNA, RIKEN full-length enriched  
DE library, clone:4933425M15 product:similar to PUTATIVE PHEROMONE  
DE RECEPTOR V2R2, full insert sequence.  
GN Name=4933425M15Rik;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;







FT	DOMAIN	746	769	Extracellular (Potential).	
FT	TRANSMEM	770	792	5 (Potential).	
FT	DOMAIN	793	805	Cytoplasmic (Potential).	
FT	TRANSMEM	806	828	6 (Potential).	
FT	DOMAIN	829	836	Extracellular (Potential).	
FT	TRANSMEM	837	862	7 (Potential).	
FT	DOMAIN	863	1079	Cytoplasmic (Potential).	
FT	CARBOHYD	90	90	N-linked (GlcNac. . .) (Potential).	
FT	CARBOHYD	130	130	N-linked (GlcNac. . .) (Potential).	
FT	CARBOHYD	261	261	N-linked (GlcNac. . .) (Potential).	
FT	CARBOHYD	287	287	N-linked (GlcNac. . .) (Potential).	
FT	CARBOHYD	386	386	N-linked (GlcNac. . .) (Potential).	
FT	CARBOHYD	446	446	N-linked (GlcNac. . .) (Potential).	
FT	CARBOHYD	468	468	N-linked (GlcNac. . .) (Potential).	
FT	CARBOHYD	488	488	N-linked (GlcNac. . .) (Potential).	
FT	CARBOHYD	541	541	N-linked (GlcNac. . .) (Potential).	
FT	CARBOHYD	594	594	N-linked (GlcNac. . .) (Potential).	
SQ	SEQUENCE	1079 AA;	120867 MW;	D7664550361F9736 CRC64;	
Query Match					34.5%; Score 1690.5; DB 1; Length 1079;
Best Local Similarity					38.0%; Pred. No. 3.9e-110;
Matches					352; Conservative 181; Mismatches 332; Indels 61; Gaps 17;
QY	18	LAFW--AELSEAKEEKEERTCRLLGKCVD	AEHNSLVIGLFPIDSR	TIPANESI-LE 74	
Db	11	LALAWSSAYGPDQRAQKGD-----	IIILGLFPIHFGVAAKDQDLKSR 54		
QY	75	PASAKCEGFNFQFRWMMKAMIMHIKEIN	KRKDILPNIITLGVQIFDTCFTISKSVEAVLVF 134		
Db	55	PESVECI RYNFGRFWLQAMIFAIEEIN	SSPSSLPNMTLGYRIFDTCNTVSKALEATLSF 114		
QY	135	LTQE---ENRPNFRNSTGAFPA--GIVGAGS	FLSVSPASRIILGLYLPQVGYTSTCVIL 189		
Db	115	VAQNKIDSLNLDKFCNCSEHIPSTIAVVG	TSGVSTAVANLLGLFYIPQVSYASSRLL 174		
QY	190	SDKYQFPSYLRIASDKIOSKAVVKRIQH	FGWVWGAIAADDDYGYGKTKFKKMESAN 249		
Db	175	SNKNQYKSFRLTIPNDEHQATAMADIEY	FRWNVGTIAADDDYGRPGIEKFREEAEERD 234		
QY	250	LCVAFSETIPKYVSNKMQKAVKAVTSTAK	VIVLYTSDIDLFLVLEMIHNITDRTWI 309		
Db	235	ICIDFSELISQSDDEEIIQOVVEVIQNST	KVIVVFSSGPDLEPLIKEIVRRNITGRWL 294		
QY	310	ATEAWITSALIAKPEYFPYGGTIGFATPR	SVIPGLKEFLDVHPNKDPNDVLTIERWQT 369		
Db	295	ASEAWASSLLIAMPEYFHVVGTTIGFLK	AGQIPGFRFLQKVHPRKSVHNGFAKEFWE 354		
QY	370	AFNCTWPNSS---VPYNVDHRVNM	TGKEDRLYDMSD---QLCTGEEKLEDLKN	TYLDTSQ 423	
Db	355	TFNCHLQEGAKGPLVDTFVRSHEEG-G	NRLLNSSTAFRPLCTGDNINSVETPYMDYEH 413		
QY	424	LRITKQCKQAVVAIAHGLDHLRSRCEG	QPGFSGNQCCAYIPFDQWLQMYMKEIKFKSH 483		
Db	414	LRISYNYLAVYSIAHALQDIYTCLPGR	GLF-TNGSCADIKKVEAWQVLKHLRHLNFTWN 472		
QY	484	EDKWVILDNDGLKNGHYDVLNWHLD-DE	GEISFVTVGRFNRSTNPFELVIPTNSTIFWN 542		
Db	473	MGEQVTFDECGDLV-GNYSIINWHLSP	EDGSIVFKEVGYNYVAKKGERLFINEEKILWS 531		
QY	543	TESSRLPHSVCTVCPPGTGRGFVQRE	PICCFDSDIPCADGHVSRKPGERECEQC	GEDYWS 602	
Db	532	GFSREVPFNSCRDCQAGTRKGIIEGE	PTCCFCEVCEPCDGEYGETDASACDKCP	DFWS 591	
QY	603	NAQSECVLKEVEYLAYDEALFTLVLS	VFGAFVLAVTAVVVIHRHTPLVNASDWJLG 662		
Db	592	NENHTSCIAKEIEFLAWTEPFGIALTL	FAVLGIFLTAFLVGVFIKFRNTPIVKATNRELS 651		
QY	663	FLIQVSLIIMLSSMLFIDKPHNWSM	AGQVTLALGFSCLCLSGTKTSSSLFLAYRISKS 722		
Db	652	YLLLFSLCCFSSSLFFIGEPQDWTCL	RQPAFGISFVLCISCLVKTNRVLLVF---EA 708		
QY	723	KTQLTSMHPLYRK-----IIVLISV	LAIEIGICTAYLILEPWPVYKNMESQNTKIILG 774		

Db	709	KIP-TSFH---RKWWGLNLQFLLVFLCT	FMQILICIWLYTAPPSSYRNHELEIIFIT 764		
QY	775	CNEISIEFLYSMFGIDAFIALLCFLTTF	VARQLPDNYVEGKITFGMLVFFIWM	SFVPV 834	
Db	765	CHEGSLMALGSLIGYTCLLAAICFFFA	FKSRKLPENFNEAKFITFSMLIFFIV	WISFIPA 824	
QY	835	YLSTKGKFMAVEIFAILASSHGLGCI	FAPKCLIIILRPERNTSEIVG	RVSTTDNCIQ 894	
Db	825	YASTYGFVSAVEVIAILAAISFGL	LACIFFNKVYIILFKPSRNTIEV--RS	STAHAHAFK 882	
QY	895	LTSAFV-----SSELNNTTVS	910		
Db	883	VAARATLRRPNISRKSSSLGGSTGS	908		
RESULT 10					
Q8J104	Q8J104	PRELIMINARY;	PRT;	1027 AA.	
AC	Q8J104;				
DT	01-OCT-2002 (TREMBlrel. 22,	Created)			
DT	01-OCT-2002 (TREMBlrel. 22,	Last sequence update)			
DT	01-MAR-2004 (TREMBlrel. 26,	Last annotation update)			
DE	Calcium polyvalent cation receptor/salinity sensing protein.				
OS	Squalus acanthias (Spiny dogfish).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;				
OC	Elasmobranchii; Squala; Hypnosqualea; Squaliformes; Squaloidei;				
OC	Squalidae; Squalus.				
OX	NCBI_TaxID=7797;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Kidney;				
RX	MEDLINE=22103704; PubMed=12093923; DOI=10.1073/pnas.152294399;				
RA	Nearing J., Betka M., Quinn S., Hentschel H., Elger M., Baum M.,				
RA	Bai M., Chattopadhyay N., Brown E.M., Hebert S.C., Harris H.W.;				
RT	"Polyvalent cation receptor proteins (Cars) are salinity sensors in				
RT	fish."				
RL	Proc. Natl. Acad. Sci. U.S.A. 99:9231-9236 (2002).				
DR	EMBL; AF406649; AAM77700.1; -.				
DR	HSSP; P23385; 1ISS.				
DR	GO; GO:0016020; C:membrane; IEA.				
DR	GO; GO:0008067; F:metabotropic glutamate, GABA-B-like recepto. . ; IEA.				
DR	GO; GO:0004872; F:receptor activity; IEA.				
DR	InterPro; IPR001828; ANF_receptor.				
DR	InterPro; IPR000068; Ca_sens_receptor.				
DR	InterPro; IPR000337; GPCR_Mgr.				
DR	InterPro; IPR011500; NCD3G_GPCR.				
DR	Pfam; PF00003; 7tm_3; 1.				
DR	Pfam; PF01094; ANF_receptor; 1.				
DR	Pfam; PF07562; NCD3G; 1.				
DR	PRINTS; PR00592; CASENSINGR.				
DR	PRINTS; PR00248; GPCRMR.				
DR	PROSITE; PS00979; G_PROTEIN_RECEP_F3_1; 1.				
DR	PROSITE; PS00980; G_PROTEIN_RECEP_F3_2; UNKNOWN_1.				
DR	PROSITE; PS00981; G_PROTEIN_RECEP_F3_3; 1.				
DR	PROSITE; PS50259; G_PROTEIN_RECEP_F3_4; 1.				
KW	Receptor.				
SQ	SEQUENCE	1027 AA;	114412 MW;	189FF1E323B5B7C7 CRC64;	
Query Match					34.4%; Score 1688.5; DB 2; Length 1027;
Best Local Similarity					38.6%; Pred. No. 5e-110;
Matches					346; Conservative 176; Mismatches 323; Indels 51; Gaps 14;
QY	53	LVIGGLFPIDSR	TIPANESI-LEPASAKCEGFNFQFRWMMKAMIMHIKEIN	KRKDILPNI 111	
Db	36	IILGLFPIHFGVAAKDQDLKSRPEATK	CIRYNFRGRFWLQAMIFAIEEINNSMTFLPNI 95		
QY	112	TLGYQIFDTCFTISKSVEAVLVLTQGE---	ENRPNFRNSTGAFPA--GIVGAGGSFLSV 166		
Db	96	TLGYRIFDTCNTVSKALEATLSFVAQN	KIDSLNLDKFCNCSDHIPSTIAVVGATGSGIST 155		
QY	167	PASRIILGLYLPQVGYTSTCVILSDKY	QFPSYLRIASDKIOSKAVVKRIQHFGWVWVGA 226		
Db	156	AVANLLGLFYIPQVSYASSRLLSNKNEY	KAFRLTIPNDEQOATAMABIEHFQWNWVGT 215		











FT	DOMAIN	863	1079	Cytoplasmic (Potential).
FT	CARBOHYD	90	90	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	130	130	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	261	261	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	287	287	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	386	386	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	446	446	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	468	468	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	488	488	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	541	541	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	594	594	N-linked (GlcNAc. . .) (Potential).
FT	VARSPLIC	461	537	Missing (in isoform B).
FT				/FTid=VSP_002036.
FT	CONFLICT	45	45	A -> S (in Ref. 2).
FT	CONFLICT	304	304	L -> P (in Ref. 3).
FT	CONFLICT	410	410	G -> D (in Ref. 2 and 3).
FT	CONFLICT	566	566	V -> A (in Ref. 2).
FT	CONFLICT	595	595	Y -> H (in Ref. 2, 3 and 5).
FT	CONFLICT	610	610	E -> V (in Ref. 5).
FT	CONFLICT	814	814	F -> L (in Ref. 5).
FT	CONFLICT	889	889	L -> I (in Ref. 2).
FT	CONFLICT	906	909	TGSN -> SGWI (in Ref. 2).
FT	CONFLICT	1057	1057	V -> M (in Ref. 2).
FT	CONFLICT	1064	1064	V -> A (in Ref. 2).
FT	CONFLICT	1076	1076	I -> V (in Ref. 2).
SQ	SEQUENCE	1079	AA; 120839	MW; AAF8D8D472736D6E CRC64;
Query Match 34.4%; Score 1685.5; DB 1; Length 1079;				
Best Local Similarity 38.0%; Pred. No. 8.7e-110;				
Matches 352; Conservative 181; Mismatches 332; Indels 61; Gaps 17;				
QY	18	LAFW--AELGSEAKEEKEERTCRLLGKCVDAENHSLVIGLFPIDSR	TIPANESI-LE 74	
Db	11	LALTWHSSAYGPDQAQKGD-----IILGGLFPIHFGVAAKDQDLKSR	54	
QY	75	PASAKCEGFNFORFRWKAMIMHIKEINKRKDILPNITLGYQIFDTCFTISKSVEAVLVF	134	
Db	55	PESVECIRYNFRGRWLQAMIFAIEEINSSPALLPNMTLGYRIFDTCNTVSKALEATLSF	114	
QY	135	LTQGE---ENRPNFRNSTGAPPA--GIVGAGGSFLSVPASRIILGYLPOVGYTSTCVIL	189	
Db	115	VAQNKIDSLNLDNDFECNCSEHIPSTIAVVGATGSGVSTAVANLLGLFYIPQVSYASSRLL	174	
QY	190	SDKYQFPSYLRVIAADKIQSKAVVRQIHFGWVWVGAIADDDYKGYGVKTFKEKMSAN	249	
Db	175	SNKNQFKSFLRTIPNDEHQATAMADIIEYFRWNWVGTTIAADDDYGRPGIEKFRFEEAERD	234	
QY	250	LCVAFSETIPKVSNEKMQKAVKVTSTAKVIVLYTSDIDISLFVLEMIHNIITDRTWI	309	
Db	235	ICIDFSELISQVSDDEEIQQVVEIQNSTAKVIVWFSSGPDLEPLIKEIVRRNITGRIWL	294	
QY	310	ATEAWITSAIAKPEYFPYFGGTIGFATPRSVIPGLKEFLYDVHPNKPNDVLTIEFWOT	369	
Db	295	ASEAWASSLIAMEYFHVVGTTIGFLKAGQIPGFRFLQVHPKRSVHNGFAKEFWEE	354	
QY	370	AFNCTWPNSS---VPYNVDHRVNMVTGKEDRLYDMSD---QLCTGEEKLEDLKNYLDTSQ	423	
Db	355	TFNCHLQDGAKGPIPVDTFVRSHEEG-GNRLNNSSTAFLRPLCTGDNINSVETPPYMGVEH	413	
QY	424	LRITKQCKQAVYIAHGLDHLRSRCEGQGFPGSNQQCAYIPTDFWQLMYMKEIKFKSH	483	
Db	414	LRISYNYLAVYSIAHALQDIYTCLPGRGLF-TNGSCADIKKVEAWQVLKHLRHLNFTWN	472	
QY	484	EDKWVILDDNGDLKNGHYDVNLWHL-DGEISFVTVGRFNRFRSTNFELVPTNSTIFWN	542	
Db	473	MGEQVTFDECGDLV-GNYSIINWHLSPEDGSIVFKEVGYNYVYAKKGERLFINEGKILWS	531	
QY	543	TESSRLPHSVCTDVCPPGTGRGVQREPICCFDSIPCADGHVSRKRPGERECEQCCEGYWS	602	
Db	532	GFSREVPFNSCRDQAGTRKGIIEGETCCFCEVCPDGEYSGETDASACDKCPDDFS	591	
QY	603	NAQKSECVLKEVEYLAYDEALGFTLVILSVFGAFVWLAVTAVVVIHRHTPLVNASDWQLG	662	

Db	592	NENYTSIAKIEFLAWTEPFGIALTLFAVLGIFLTAFLVGLGVFIKFRNTPIVKATNRELS	655
Qy	663	FLIQVSLIIMLLSSMLFIDKPHNWSMAGQVTLALGFSLCLSLGKTSLLFLAYRISKS	722
Db	652	YLLLFSLCCFSSSLFFIGEPQDWTCLRLQPAFGISFVLCISCLLVKTNRVLLVF---EA	708
Qy	723	KTQLTSMHPLYRK-----IIVLISVLAIEIGICTAYLILEPPMVYKNMESQNTKIILG	774
Db	709	KIP-TSFH--RKWWGLNLQFLLVFLCTFMQIVICIIWLVTAPSSYRNHELEDEIIFIT	764
Qy	775	CNEISIEFLYSMFGIDAFALLCFLTTFVARQLPDNYYEGKCTIFGMLVFFIWMVSFVPV	834
Db	765	CHGSLMALGSLIGYTCLLAAICFFFAFKSRKLPENFNEAKFITFSMLIFFIVWISFIPA	824
Qy	835	YLSTGKPKMAVEIFAILASSHGLLGCIFAPKAPKCLIIILLRPENTSEIVCGRVSTTDNCIQ	894
Db	825	YASTYGKFVSAVEVIALAASFGLLACIFFNKKVYIILFKPSRNTIEEV--RSSTAHAHAFK	882
Qy	895	LTSAFV-----SSELNNTTVS	910
Db	883	VAARATLRRPNISRKRSSSLGGSTGS	908
RESULT 13			
Q90WL6			
ID	Q90WL6	PRELIMINARY;	PRT; 940 AA.
AC	Q90WL6;		
DT	01-DEC-2001	(Tremblrel. 19, Created)	
DT	01-DEC-2001	(Tremblrel. 19, Last sequence update)	
DT	01-JUN-2003	(Tremblrel. 24, Last annotation update)	
DE	Extracellular calcium sensing receptor.		
GN	Name=casr;		
OS	Sparus aurata (Gilthead sea bream).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;		
OC	Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Percoidae;		
OC	Sparidae; Sparus.		
OX	NCBI_TaxID=8175;		
RN	{1}		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=21930045; PubMed=119322208;		
RA	Clark M.S., Bendell L., Power D.M., Warner S., Elgar G.,		
RA	Ingleton P.M.;		
RT	"Calcitonin: Characterisation and expression in a Teleost fish: Fugu		
RT	rubripes.";		
RL	J. Mol. Endocrinol. 28:111-123 (2002).		
DR	EMBL; AJ289717; CAC41352.1; -.		
DR	HSSP; P23385; IEWK.		
DR	GO; GO:0016020; C:membrane; IEA.		
DR	GO; GO:0008067; F:metabotropic glutamate, GABA-B-like recepto. . .; IEA.		
DR	GO; GO:0004872; F:receptor activity; IEA.		
DR	pfam; PF00003; 7tm_3; 1.		
DR	pfam; PF01094; ANF_receptor; 1.		
DR	pfam; PF07562; NCD3G; 1.		
DR	PRINTS; PR00592; CASENSINGR.		
DR	PRINTS; PR00248; GPCRMR.		
DR	PROSITE; PS00979; G_PROTEIN_RECEP_F3_1; 1.		
DR	PROSITE; PS50259; G_PROTEIN_RECEP_F3_4; 1.		
KW	Receptor.		
SQ	SEQUENCE 940 AA; 105455 MW; 19C3CEDC75A0E3F9 CRC64;		
Query Match 33.2%; Score 1630.5; DB 2; Length 940;			
Best Local Similarity 37.9%; Pred. No. 5.5e-106;			
Matches 337; Conservative 164; Mismatches 330; Indels 59; Gaps 14			
Qy	53	LVIGGLFPIDSR	TIPANESI-LEPASAKCEGFNFORFRWKAMIMHIKEINKRKDILPNI 111
Db	32	ILLGGLFPIHFGVASKDQDLAARPESSQCVRNFRGFRWLQAMIFAIDEINSSLTLLPNI	91
Qy	112	TILGYQIFDTCFTISKSVEAVLVLTGQE---ENRPNFRNSTGAPPA--GIVGAGGSFLSV	166
Db	92	TILGYRIFDTCNTVSKALEATLSFVAQNKIDSLNLDNDFCNCTDHPATIAVWGAAGSAVST	151



Db	786	TEAKFITFSMLIFFIIVWISFIPAYFSTYKGFVSAVEVIAILASSFGLLACIFFNKVYIIL	845
QY	872	LRPERNTSEIVCGRVSTTDNCIQLTS	897
Db	846	FKPSRNTIEEV--RCSTAHSFKVAA	869
RESULT 15			
Q6XAF3	PRELIMINARY; PRT; 941 AA.		
ID	Q6XAF3		
AC	Q6XAF3;		
DT	05-JUL-2004 (TremBLrel. 27, Created)		
DT	05-JUL-2004 (TremBLrel. 27, Last sequence update)		
DT	05-JUL-2004 (TremBLrel. 27, Last annotation update)		
DE	Calcium polyvalent cation receptor 2.		
OS	Salmo salar (Atlantic salmon).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Actinopterygii; Neopterygii; Teleostei; Euteleostei;		
OC	Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.		
OX	NCBI_TaxID=8030;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Kidney;		
RA	Nearing J.A.; Harris W.;		
RL	Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AY245443; AAP79923.1; --		
DR	GO; GO:0016020; C:membrane; IEA.		
DR	GO; GO:0008067; F:metabotropic glutamate, GABA-B-like recepto. . .; IEA.		
DR	GO; GO:0004872; F:receptor activity; IEA.		
DR	InterPro; IPR001828; ANF_receptor.		
DR	InterPro; IPR000068; Ca_sens_receptor.		
DR	InterPro; IPR000337; GPCR_Mgr.		
DR	InterPro; IPR011500; NCD3G_GPCR.		
DR	Pfam; PF00003; 7tm_3; 1.		
DR	Pfam; PF01094; ANF_receptor; 1.		
DR	Pfam; PF07562; NCD3G; 1.		
DR	PRINTS; PR00592; CASENSINGR.		
DR	PRINTS; PR00248; GPCRMRGR.		
DR	PROSITE; PS00979; G_PROTEIN_RECEP_F3_1; 1.		
DR	PROSITE; PS50259; G_PROTEIN_RECEP_F3_4; 1.		
KW	Receptor.		
SQ	SEQUENCE 941 AA; 106072 MW; C72B91C0029DFF27 CRC64;		
Query Match 33.2%; Score 1629.5; DB 2; Length 941;			
Best Local Similarity 38.3%; Pred. No. 6.4e-106;			
Matches 332; Conservative 168; Mismatches 317; Indels 49; Gaps 13			
QY	53	LVIGGLFPIDSRTPANESI-LEPASAKCEGFNFQFRWMKAMIHMIKEINKRKDILPNI	111
Db	32	ILGLGFPMHFGVTSKDQDLAARPESTECVRYNFRGRWLQAMIFAIEEINNSSTLLPNI	91
QY	112	TLGYQIFDTCFTISKVSAVLVLTQGE---ENRPNFRNSTGAPPA--GIVGAGGSFLSV	166
Db	92	TLGYRIFDTCNTVSKALEATLSFVAQNKIDSLNDEFNCNCTDHPSTIAVVGASGSAVST	151
QY	167	PASRILGLYLPQVGYTSTCVILSDKYQFPSPYLRVIAASDKIQSKAVVKRIQHFGWVWGA	226
Db	152	AVANLLGLFYIPQISYASSRLLSNKNQFKSFMRTIPTDEHQATAMADIIDYFQWNVVIA	211
QY	227	IAADDDYKGYVKTFKEKMESANLCVAFSETIPKVYSNEKMQKAVKAVKTSTAKVIVLYT	286
Db	212	VASDDEYGRPGIEKFEKEMEERDICIHLSELISQYFEEWQIQLVGRIENTSSAKVIVVFA	271
QY	287	SDIDLSLFVLEMIHNNITDRTWIATEAWITSALIAKPEYFPYFGGTIGFATPRSVIPGLK	346
Db	272	SGPDIEPLIKMVRNRNITDRIWLASEAWATTSLIAKPEYLDVVVGTIGFALRAGEIPGFK	331
QY	347	EFLYDVHPNKPNDVLTIEFWQAFNCTWPNSSVPYNVDHRVNMVGKEDRLYDMSD----	402
Db	332	DFLQEVTPKSSHNEFVREFWEETFNCYLEDS-----QRLRDSENGSTS	375
QY	403	--QLCTGEEKLEDLKNYLTDSQLRITKQCKQAVYIAHGLDHLSRCQEGQGPGFGSNQQC	460

Db	376	FRPLCTGEEDIMGAETPYLDYTHLRISYNNVYVAVHSIAQALQDILTCIPGRGLF-SNNSC	434
QY	461	AVIPTDFWQLMYMKEIKFKSHEDKWVILDDNGDLKNGHYDVLNWHLD-DEGEISFVTV	519
Db	435	ADIKKIEAWQVLKQLRHLNFNSMGEKVHFDENAD-PSGNYTIINWHRSPEDGWSVFEEV	493
QY	520	GRFNERSTNFEVIPNTSTIFWNTESSRLPHSVCTDVCPPGTRGFRVQREPICCFDSIPC	579
Db	494	GFYNMRAKRGVQLFIDNTKILWNGYNTTEVPFNSCEDCEPGTRKGIIESMPTCCPECTEC	553
QY	580	ADGHVSRKPGERECEQCCEGYMSNAQKSECVLKEVEYLAYDEALGFTLVILSVFGAFVVL	639
Db	554	SEGEYSCHKDASVCTKCPNDSWSENHTSCFLKEIEFLSWTEPFGIALALCSVLGVFLTA	613
QY	640	AVTAVVVIHRHTPLVNASDWQLGFLIOVSLIIMLLSSMLFIDKPHNWSMAGQVTLALGF	699
Db	614	FVMGVFIKFRNTPIVKATNRELSYLLLFSLICCFSSSLIFIGEPQDWTCLRLRQAPAGISF	673
QY	700	SLCLSCLLGKTSSFLAYRISKSTQLTSMHPLYRK-----IIVLISVLAIEIGICTA	751
Db	674	VLCISILVKTNRVLLVE-AKIPTS-----LHRKMWGLNLQFLLVFLFTFVQVMICVW	726
QY	752	YLILEPPMVYKNMESQNTKIILGCNEISIEFLYSMFGIDAFIALLCFLTTFVARQLPDNY	811
Db	727	WLYNAPPASYRNHDIDEI-IFITCNEGSMMALGFLIGYTCLLAAICFFFAFKSRKLPENF	785
QY	812	YEGKCITFGMLVFFIIMSFVPVYVYSTKGKFMAVEIFAILASSHGLLGICIFAPKCLIL	871
Db	786	TEAKFITFSMLIFFIIVWISFIPAYFSTYKGFVSAVEVIAILASSFGLLACIFFNKVYIIL	845
QY	872	LRPERNTSEIVCGRVSTTDNCIQLTS	897
Db	846	FKPSRNTIEEV--RCSTAHSFKVAA	869

Search completed: February 16, 2005, 16:36:48  
Job time : 171.877 secs